SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Baker, Joffre
Chien, Kenneth
King, Kathleen
Pennica, Diane
Wood, William

(ii) TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 460 Point San Bruno Blvd
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: patin (Genentech)

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: 05-AUG-1994
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/233609
(B) FILING DATE: 25-APR-1994

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Hasak, Janet E.
(B) REGISTRATION NUMBER: 28,616
(C) REFERENCE/DOCKET NUMBER: 894P1

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 415/225-1896
(B) TELEFAX: 415/952-9881
(C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1352 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGATAAGCCT GGGGCCAGCA TGAGCCAGAG GGAGGGAAGT CTGGAAGACC 50

ACCAGACTGA CTCCTCAATC TCATTCCTAC CCCATTTGGA GGCCAAGATC 100

CGCCAGACAC ACAACCTTGC CCGCCTCCTG ACCAAATATG CAGAACAACT 150

TCTGGAGGAA TACGTGCAGC AACAGGGAGA GCCCTTTGGG CTGCCGGGCT 200

TCTCACCACC GCGGCTGCCG CTGGCCGGCC TGAGTGGCCC GGCTCCGAGC 250

CATGCAGGGC TACCGGTGTC CGAGCGGCTG CGGCAGGATG CAGCCGCCCT 300

GAGTGTGCTG CCCGCGCTGT TGGATGCCGT CCGCCGCCGC CAGGCGGAGC 350

TGAACCCGCG CGCCCCGCGC CTGCTGCGGA GCCTGGAGGA CGCAGCCCGC 400

CAGGTTCGGG CCCTGGGCGC CGCGGTGGAG ACAGTGCTGG CCGCGCTGGG 450

CGCTGCAGCC CGCGGGCCCG GCCAGAGCC CGTCACCGTC GCCACCCTCT 500

TCACGGCCAA CAGCACTGCA GGCATCTTCT CAGCCAAGGT GCTGGGGTTC 550

CACGTGTGCG GCCTCTATGG CGAGTGGGTG AGCCGCACAG AGGGCGACCT 600

GGGCCAGCTG GTGCCAGGGG GCGTCGCCTG AGAGTGAATA CTTTTTCTTG 650

TAAGCTCGCT CTGTCTCGCC TCTTTGGCTT CAAATTTTCT GTCTCTCCAT 700

CTGTGTCCTG TGTGTTCTTG GGCTGTCCCT ATCTTTCTGC ATTTGTGTGG 750

TCTCTCTCTT CTGCTCTCCT CTCTGCAGGG AGCTTCTTTT TTCCAACAGT 800

TTCTCGTTTT GTCTCTCTCC AGTCTTGAAC ACTTTTGTCT CCGAGAGGTC 850

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TCTTTTTGTT TCCTTGTCTC TTGGTTCTTT CTTTGCTTGC TTGCTTGCTT 900

GCTTGCTTGT TGTTGAGACA GGGTCTCACC ATATAGCTCT GGATGGCCTG 950

GAACTTGCTA TGTAGGCCAG GCTGGCCTCC AGCTCATAGA GATCCACTTG 1000

CCTCCGACTC CCAATTTCCC CATCTGTCTC CCTGTGATCC ATATGGGTAT 1050

GTGTAACCCT TACTTTGTCT CATGGAGGTG ACAATTTTTC TCCCTTCAGT 1100

TTCTTTGTTC TTTACTGACC AGAAAGTGC CTACTTGTCC CCTGGTGGCA 1150

AGGCCATTCA CCTTAGGACC TTCCCACCAG TTCCTTTGTA GGCAAATCCC 1200

TCCCCCTTTG AGGTCCTTCC CTTTCATACC GCCCTAGGCT GGTCAATGGA 1250

GAGAGAAAGG CAGAAAAACA TCTTTAAAGA GTTTTATTTG AGAATAAATT 1300

AATTTTTGTA AATAAAATGT TTAACAATAA AACTAAACTT TTATGAAAAA 1350

AA 1352

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1352 bases
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCTATTCGGA CCCCGGTCGT ACTCGGTCTC CCTCCCTTCA GACCTTCTGG 50

TGGTCTGACT GAGGAGTTAG AGTAAGGATG GGGTAAACCT CCGGTTCTAG 100

GCGGTCTGTG TGTTGGAACG GGCGGAGGAC TGGTTTATAC GTCTTGTTGA 150

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AGACCTCCTT ATGCACGTCG TTGTCCCTCT CGGGAAACCC GACGGCCCGA 200

AGAGTGGTGG CGCCGACGGC GACCGGCCGG ACTCACCGGG CCGAGGCTCG 250

GTACGTCCCG ATGGCCACAG GCTCGCCGAC GCCGTCCTAC GTCGGCGGGA 300

CTCACACGAC GGGCGCGACA ACCTACGGCA GGCGGCGGCG GTCCGCCTCG 350

ACTTGGGCGC GCGGGGCGCG GACGACGCCT CGGACCTCCT GCGTCGGGCG 400

GTCCAAGCCC GGGACCCGCG GCGCCACCTC TGTCACGACC GGCGCGACCC 450

GCGACGTCGG GCGCCCGGGC CCGGTCTCGG GCAGTGGCAG CGGTGGGAGA 500

AGTGCCGGTT GTCGTGACGT CCGTAGAAGA GTCGGTTCCA CGACCCCAAG 550

GTGCACACGC CGGAGATACC GCTCACCCAC TCGGCGTGTC TCCCGCTGGA 600

CCCGGTCGAC CACGGTCCCC CGCAGCGGAC TCTCACTTAT GAAAAGAAC 650

ATTCGAGCGA GACAGAGCGG AGAAACCGAA GTTTAAAAGA CAGAGAGGTA 700

GACACAGGAC ACACAAGAAC CCGACAGGGA TAGAAAGACG TAAACACACC 750

AGAGAGAGAA GACGAGAGGA GAGACGTCCC TCGAAGAAAA AAGGTTGTCA 800

AAGAGCAAAA CAGAGAGAGG TCAGAACTTG TGAAAACAGA GGCTCTCCAG 850

AGAAAAACAA AGGAACAGAG AACCAAGAAA GAAACGAACG AACGAACGAA 900

CGAACGAACA ACAACTCTGT CCCAGAGTGG TATATCGAGA CCTACCGGAC 950

CTTGAACGAT ACATCCGGTC CGACCGGAGG TCGAGTATCT CTAGGTGAAC 1000

GGAGGCTGAG GGTTAAAGGG GTAGACAGAG GGACACTAGG TATACCCATA 1050

CACATTGGGA ATGAAACAGA GTACCTCCAC TGTTAAAAAG AGGGAAGTCA 1100

AAGAAACAAG AAATGACTGG TCTTTTCACG GATGAACAGG GGACCACCGT 1150

TCCGGTAAGT GGAATCCTGG AAGGGTGGTC AAGGAAACAT CCGTTTAGGG 1200

AGGGGGAAAC TCCAGGAAGG GAAAGTATGG CGGGATCCGA CCAGTTACCT 1250

CTCTCTTTCC GTCTTTTTGT AGAAATTTCT CAAAATAAAC TCTTATTTAA 1300

TTAAAAACAT TTATTTTACA AATTGTTATT TTGATTTGAA AATACTTTTT 1350

TT 1352

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 203 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

    Met Ser Gln Arg Glu Gly Ser Leu Glu Asp His Gln Thr Asp Ser
    1   5   10   15

    Ser Ile Ser Phe Leu Pro His Leu Glu Ala Lys Ile Arg Gln Thr
                    20   25   30

    His Asn Leu Ala Arg Leu Leu Thr Lys Tyr Ala Glu Gln Leu Leu
                    35   40   45

    Glu Glu Tyr Val Gln Gln Gln Gly Glu Pro Phe Gly Leu Pro Gly
                    50   55   60

    Phe Ser Pro Pro Arg Leu Pro Leu Ala Gly Leu Ser Gly Pro Ala
                    65   70   75

    Pro Ser His Ala Gly Leu Pro Val Ser Glu Arg Leu Arg Gln Asp
                    80   85   90

    Ala Ala Ala Leu Ser Val Leu Pro Ala Leu Leu Asp Ala Val Arg
                    95   100   105

    Arg Arg Gln Ala Glu Leu Asn Pro Arg Ala Pro Arg Leu Leu Arg
                    110   115   120

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Ser Leu Glu Asp Ala Ala Arg Gln Val Arg Ala Leu Gly Ala Ala
125 130 135

Val Glu Thr Val Leu Ala Ala Leu Gly Ala Ala Arg Gly Pro
140 145 150

Gly Pro Glu Pro Val Thr Val Ala Thr Leu Phe Thr Ala Asn Ser
155 160 165

Thr Ala Gly Ile Phe Ser Ala Lys Val Leu Gly Phe His Val Cys
170 175 180

Gly Leu Tyr Gly Glu Trp Val Ser Arg Thr Glu Gly Asp Leu Gly
185 190 195

Gln Leu Val Pro Gly Gly Val Ala
200 203

(2) INFORMATION FOR SEQ ID NO:4:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 200 amino acids
     (B) TYPE: amino acid
     (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Phe Thr Glu His Ser Pro Leu Thr Pro His Arg Arg Asp
1 5 10 15

Leu Cys Ser Arg Ser Ile Trp Leu Ala Arg Lys Ile Arg Ser Asp
20 25 30

Leu Thr Ala Leu Thr Glu Ser Tyr Val Lys His Gln Gly Leu Asn
35 40 45

Lys Asn Ile Asn Leu Asp Ser Ala Asp Gly Met Pro Val Ala Ser
50 55 60

Thr Asp Gln Trp Ser Glu Leu Thr Glu Ala Glu Arg Leu Gln Glu
65 70 75

Asn Leu Gln Ala Tyr Arg Thr Phe His Val Leu Leu Ala Arg Leu
80 85 90

Leu Glu Asp Gln Gln Val His Phe Thr Pro Thr Glu Gly Asp Phe
95 100 105

His Gln Ala Ile His Thr Leu Leu Leu Gln Val Ala Ala Phe Ala
110 115 120

Tyr Gln Ile Glu Glu Leu Met Ile Leu Leu Glu Tyr Lys Ile Pro
125 130 135

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        Arg Asn Glu Ala Asp Gly Met Pro Ile Asn Val Gly Asp Gly Gly
                        140             145                     150

  5     Leu Phe Glu Lys Lys Leu Trp Gly Leu Lys Val Leu Gln Glu Leu
                        155             160                     165

        Ser Gln Trp Thr Val Arg Ser Ile His Asp Leu Arg Phe Ile Ser
                        170             175                     180

 10     Ser His Gln Thr Gly Ile Pro Ala Arg Gly Ser His Tyr Ile Ala
                        185             190                     195

        Asn Asn Lys Lys Met
                        200
 15
        (2) INFORMATION FOR SEQ ID NO:5:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 50 bases
 20             (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
 25

      GCGGCCGCGA GCTCGAATTC TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT 50

 30
        (2) INFORMATION FOR SEQ ID NO:6:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 1018 bases
 35             (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
 40

      GTGAAGGGAG CCGGGATCAG CCAGGGGCCA GCATGAGCCG GAGGGAGGGA 50

 45   AGTCTGGAAG ACCCCCAGAC TGATTCCTCA GTCTCACTTC TTCCCCACTT 100

      GGAGGCCAAG ATCCGTCAGA CACACAGCCT TGCGCACCTC CTCACCAAAT 150

 50
      ACGCTGAGCA GCTGCTCCAG GAATATGTGC AGCTCCAGGG AGACCCCTTC 200

      GGGCTGCCCA GCTTCTCGCC GCCGCGGCTG CCGGTGGCCG GCCTGAGCGC 250
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CCCGGCTCCG AGCCACGCGG GGCTGCCAGT GCACGAGCGG CTGCGGCTGG 300

ACGCGGCGGC GCTGGCCGCG CTGCCCCCGC TGCTGGACGC AGTGTGTCGC 350

CGCCAGGCCG AGCTGAACCC GCGCGCGCCG CGCCTGCTGC GCCGCCTGGA 400

GGACGCGGCG CGCCAGGCCC GGGCCCTGGG CGCCGCCGTG GAGGCCTTGC 450

TGGCCGCGCT GGGCGCCGCC AACCGCGGGC CCGGGCCGA GCCCCCGCC 500

GCCACCGCCT CAGCCGCCTC CGCCACCGGG GTCTTCCCCG CCAAGGTGCT 550

GGGGCTCCGC GTTTGCGGCC TCTACCGCGA GTGGCTGAGC CGCACCGAGG 600

GCGACCTGGG CCAGCTGCTG CCCGGGGGCT CGGCCTGAGC GCCGCGGGGC 650

AGCTCGCCCC GCCTCCTCCC GCTGGGTTCC GTCTCTCCTT CCGCTTCTTT 700

GTCTTTCTCT GCCGCTGTCG GTGTCTGTCT GTCTGCTCTT AGCTGTCTCC 750

ATTGCCTCGG CCTTCTTTGC TTTTTGTGGG GGAGAGGGGA GGGGACGGGC 800

AGGGTCTCTG TCGCCCAGGC TGGGGTGCAG TGGCGCGATC CCAGCACTGC 850

AGCCTCAACC TCCTGGGCTC AAGCCATCCT TCCGCCTCAG CTTCCCCAGC 900

AGCTGGGACT ACAGGCACGC GCCACCACAG CCGGCTAATT TTTTATTTAA 950

TTTTTTGTAG AGACGAGGTT TCGCCATGTT GCCCAGGCTG GTCTTGAACT 1000

CCGGGGCTCA AGCGATCC 1018

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 1018 bases

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(B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CACTTCCCTC GGCCCTAGTC GGTCCCCGGT CGTACTCGGC CTCCCTCCCT 50

TCAGACCTTC TGGGGGTCTG ACTAAGGAGT CAGAGTGAAG AAGGGGTGAA 100

CCTCCGGTTC TAGGCAGTCT GTGTGTCGGA ACGCGTGGAG GAGTGGTTTA 150

TGCGACTCGT CGACGAGGTC CTTATACACG TCGAGGTCCC TCTGGGGAAG 200

CCCGACGGGT CGAAGAGCGG CGGCGCCGAC GGCCACCGGC CGGACTCGCG 250

GGGCCGAGGC TCGGTGCGCC CCGACGGTCA CGTGCTCGCC GACGCCGACC 300

TGCGCCGCCG CGACCGGCGC GACGGGGGCG ACGACCTGCG TCACACAGCG 350

GCGGTCCGGC TCGACTTGGG CGCGCGCGGC GCGGACGACG CGGCGGACCT 400

CCTGCGCCGC GCGGTCCGGG CCCGGGACCC GCGGCGGCAC CTCCGGAACG 450

ACCGGCGCGA CCCGCGGCGG TTGGCGCCCG GGGCCCGGCT CGGGGGGCGG 500

CGGTGGCGGA GTCGGCGGAG GCGGTGGCCC CAGAAGGGGC GGTTCCACGA 550

CCCCGAGGCG CAAACGCCGG AGATGGCGCT CACCGACTCG GCGTGGCTCC 600

CGCTGGACCC GGTCGACGAC GGGCCCCCGA GCCGGACTCG CGGCGCCCCG 650

TCGAGCGGGG CGGAGGAGGG CGACCCAAGG CAGAGAGGAA GGCGAAGAAA 700

CAGAAAGAGA CGGCGACAGC CACAGACAGA CAGACGAGAA TCGACAGAGG 750

TAACGGAGCC GGAAGAAACG AAAAACACCC CCTCTCCCCT CCCCTGCCCG 800

                                -119-

TCCCAGAGAC AGCGGGTCCG ACCCCACGTC ACCGCGCTAG GGTCGTGACG 850

TCGGAGTTGG AGGACCCGAG TTCGGTAGGA AGGCGGAGTC GAAGGGGTCG 900

TCGACCCTGA TGTCCGTGCG CGGTGGTGTC GGCCGATTAA AAAATAAATT 950

AAAAAACATC TCTGCTCCAA AGCGGTACAA CGGGTCCGAC CAGAACTTGA 1000

GGCCCCGAGT TCGCTAGG 1018

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 201 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ser Arg Arg Glu Gly Ser Leu Glu Asp Pro Gln Thr Asp Ser
1   5   10   15

Ser Val Ser Leu Leu Pro His Leu Glu Ala Lys Ile Arg Gln Thr
             20   25   30

His Ser Leu Ala His Leu Leu Thr Lys Tyr Ala Glu Gln Leu Leu
             35   40   45

Gln Glu Tyr Val Gln Leu Gln Gly Asp Pro Phe Gly Leu Pro Ser
             50   55   60

Phe Ser Pro Pro Arg Leu Pro Val Ala Gly Leu Ser Ala Pro Ala
             65   70   75

Pro Ser His Ala Gly Leu Pro Val His Glu Arg Leu Arg Leu Asp
             80   85   90

Ala Ala Ala Leu Ala Ala Leu Pro Pro Leu Leu Asp Ala Val Cys
             95   100   105

Arg Arg Gln Ala Glu Leu Asn Pro Arg Ala Pro Arg Leu Leu Arg
             110   115   120

Arg Leu Glu Asp Ala Ala Arg Gln Ala Arg Ala Leu Gly Ala Ala
             125   130   135

Val Glu Ala Leu Leu Ala Ala Leu Gly Ala Ala Asn Arg Gly Pro
             140   145   150

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    Arg Ala Glu Pro Pro Ala Ala Thr Ala Ser Ala Ala Ser Ala Thr
                    155             160             165

5   Gly Val Phe Pro Ala Lys Val Leu Gly Leu Arg Val Cys Gly Leu
                    170             175             180

    Tyr Arg Glu Trp Leu Ser Arg Thr Glu Gly Asp Leu Gly Gln Leu
                    185             190             195

10  Leu Pro Gly Gly Ser Ala
                    200 201
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